

OSTO 01/02 OIPE
 CRF Processing Date: 1/15/2002 3:29 PM
 Edited by: [Signature]
 Verified by: [Signature] (STIC Staff)

Serial Number: 09/918,026A

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

OIPE

RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/918,026A

TIME: 20:21:04

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01152002\I918026A.raw

4 <110> APPLICANT: Rosanne M. Crooke
 5 Mark J. Graham
 6 Kristina M. Lemonidis
 9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COA CHOLESTEROL
 ACYLTRANSFERASE-2 EXPRESSION
 11 <130> FILE REFERENCE: ISPH-0588
 13 <140> CURRENT APPLICATION NUMBER: US/09/918,026A
 14 <141> CURRENT FILING DATE: 2001-07-30
 16 <160> NUMBER OF SEQ ID NOS: 65
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 20
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Artificial Sequence
 23 <220> FEATURE:
 24 <223> OTHER INFORMATION: Antisense Oligonucleotide
 26 <400> SEQUENCE: 1
 27 tccgtcatcg ctctcaggg 20
 29 <210> SEQ ID NO: 2
 30 <211> LENGTH: 20
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Artificial Sequence
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: Antisense Oligonucleotide
 37 <400> SEQUENCE: 2
 38 atgcattctg cccccaagga 20
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 1569
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Homo sapiens
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (1)...(1569)
 49 <400> SEQUENCE: 3
 50 atg gag cca ggc ggg gcc cgt ctg cgt ctg cag agg aca gaa ggg ctg 48
 51 Met Glu Pro Gly Gly Ala Arg Leu Arg Leu Gln Arg Thr Glu Gly Leu
 52 1 5 10 15
 54 gga ggg gag cgg gag cgc caa ccc tgt gga gat gga aac act gag acg 96
 55 Gly Gly Glu Arg Glu Arg Gln Pro Cys Gly Asp Gly Asn Thr Glu Thr
 56 20 25 30
 58 cac aga gcc ccg gac ttg gta caa tgg acc cga cac atg gag gct gtg 144
 59 His Arg Ala Pro Asp Leu Val Gln Trp Thr Arg His Met Glu Ala Val
 60 35 40 45
 62 aag gca caa ttg ctg gag caa gcg cag gga caa ctg agg gag ctg ctg 192
 63 Lys Ala Gln Leu Leu Glu Gln Ala Gln Gly Gln Leu Arg Glu Leu Leu
 64 50 55 60
 66 gat cgg gcc atg cgg gag gct ata caa tcc tac cca tca caa gac aaa 240
 67 Asp Arg Ala Met Arg Glu Ala Ile Gln Ser Tyr Pro Ser Gln Asp Lys
 68 65 70 75 80

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70 cct ctg ccc cca cct ccc cca ggt tcc ttg agc agg acc cag gag cca 288
71 Pro Leu Pro Pro Pro Pro Gly Ser Leu Ser Arg Thr Gln Glu Pro
72      85      90      95
74 tcc ctg ggg aaa cag aaa gtt ttc atc atc cgc aag tcc ctg ctt gat 336
75 Ser Leu Gly Lys Gln Lys Val Phe Ile Ile Arg Lys Ser Leu Leu Asp
76      100      105      110
78 gag ctg atg gag gtg cag cat ttc cgc acc atc tac cac atg ttc atc 384
79 Glu Leu Met Glu Val Gln His Phe Arg Thr Ile Tyr His Met Phe Ile
80      115      120      125
82 gct ggc ctg tgt gtc ttc atc atc agc acc ctg gcc atc gac ttc att 432
83 Ala Gly Leu Cys Val Phe Ile Ile Ser Thr Leu Ala Ile Asp Phe Ile
84      130      135      140
86 gat gag ggc agg ctg ctg ctg gag ttt gac cta ctg atc ttc agc ttc 480
87 Asp Glu Gly Arg Leu Leu Leu Glu Phe Asp Leu Leu Ile Phe Ser Phe
88 145      150      155      160
90 gga cag ctg cca ttg gcg ctg gtg acc tgg gtg ccc atg ttt ctg tcc 528
91 Gly Gln Leu Pro Leu Ala Leu Val Thr Trp Val Pro Met Phe Leu Ser
92      165      170      175
94 acc ctg ttg gcg ccg tac cag gcc cta cgg ctg tgg gcc agg ggc acc 576
95 Thr Leu Leu Ala Pro Tyr Gln Ala Leu Arg Leu Trp Ala Arg Gly Thr
96      180      185      190
98 tgg acg cag gcg acg ggc ctg ggc tgt gcg ctt tta gcc gcc cac gcc 624
99 Trp Thr Gln Ala Thr Gly Leu Gly Cys Ala Leu Leu Ala Ala His Ala
100      195      200      205
102 gtg gtg ctc tgc gcg ctg ccg gtc cac gtg gcc gtg gag cat cag ctc 672
103 Val Val Leu Cys Ala Leu Pro Val His Val Ala Val Glu His Gln Leu
104      210      215      220
106 ccg ccg gcc tcc cgt tgt gtc ctg gtc ttc gag cag gtt agg ttc ctg 720
107 Pro Pro Ala Ser Arg Cys Val Leu Val Phe Glu Gln Val Arg Phe Leu
108 225      230      235      240
110 atg aaa agc tac tcc ttc ctg aga gag gct gtg cct ggg atc ctt cgt 768
111 Met Lys Ser Tyr Ser Phe Leu Arg Glu Ala Val Pro Gly Ile Leu Arg
112      245      250      255
114 gcc aga cga ggt gag ggg atc cag gcc ccc agt ttc tcc agc tac ctc 816
115 Ala Arg Arg Gly Glu Gly Ile Gln Ala Pro Ser Phe Ser Ser Tyr Leu
116      260      265      270
118 tac ttc ctc ttc tgc cca aca ctc atc tac agg gag act tac cct agg 864
119 Tyr Phe Leu Phe Cys Pro Thr Leu Ile Tyr Arg Glu Thr Tyr Pro Arg
120      275      280      285
122 acg ccc tat gtc agg tgg aat tat gtg gcc aag aac ttt gcc cag gcc 912
123 Thr Pro Tyr Val Arg Trp Asn Tyr Val Ala Lys Asn Phe Ala Gln Ala
124      290      295      300
126 ctg gga tgt gtg ctc tat gcc tgc ttc atc ctg ggc cgc ctc tgt gtt 960
127 Leu Gly Cys Val Leu Tyr Ala Cys Phe Ile Leu Gly Arg Leu Cys Val
128 305      310      315      320
130 cct gtc ttt gcc aac atg agc cga gag ccc ttc agc acc cgt gcc ctg 1008
131 Pro Val Phe Ala Asn Met Ser Arg Glu Pro Phe Ser Thr Arg Ala Leu
132      325      330      335
134 gtg ctc tct atc ctg cat gcc acg ttg cca ggc atc ttc atg ctg ctg 1056

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135 Val Leu Ser Ile Leu His Ala Thr Leu Pro Gly Ile Phe Met Leu Leu
136          340          345          350
138 ctc atc ttc ttt gcc ttc ctc cat tgc tgg ctc aac gcc ttt gcc gag 1104
139 Leu Ile Phe Phe Ala Phe Leu His Cys Trp Leu Asn Ala Phe Ala Glu
140          355          360          365
142 atg cta cga ttt gga gac agg atg ttc tac cgg gac tgg tgg aac tca 1152
143 Met Leu Arg Phe Gly Asp Arg Met Phe Tyr Arg Asp Trp Trp Asn Ser
144          370          375          380
146 acg tcc ttc tcc aac tac tac cgc act tgg aac gtg gtg gtc cat gac 1200
147 Thr Ser Phe Ser Asn Tyr Tyr Arg Thr Trp Asn Val Val Val His Asp
148 385          390          395          400
150 tgg ctg tac agc tac gtg tat cag gat ggg ctg cgg ctc ctt ggt gcc 1248
151 Trp Leu Tyr Ser Tyr Val Tyr Gln Asp Gly Leu Arg Leu Leu Gly Ala
152          405          410          415
154 cgg gcc cga ggg gta gcc atg ctg ggt gtg ttc ctg gtc tcc gca gtg 1296
155 Arg Ala Arg Gly Val Ala Met Leu Gly Val Phe Leu Val Ser Ala Val
156          420          425          430
158 gcc cat gag tat atc ttc tgc ttc gtc ctg ggg ttc ttc tat ccc gtc 1344
159 Ala His Glu Tyr Ile Phe Cys Phe Val Leu Gly Phe Phe Tyr Pro Val
160          435          440          445
162 atg ctg ata ctc ttc ctt gtc att gga gga atg ttg aac ttc atg atg 1392
163 Met Leu Ile Leu Phe Leu Val Ile Gly Gly Met Leu Asn Phe Met Met
164          450          455          460
166 cat gac cag cgc acc ggc ccg gca tgg aac gtg ctg atg tgg acc atg 1440
167 His Asp Gln Arg Thr Gly Pro Ala Trp Asn Val Leu Met Trp Thr Met
168 465          470          475          480
170 ctg ttt cta ggc cag gga atc cag gtc agc ctg tac tgc cag gag tgg 1488
171 Leu Phe Leu Gly Gln Gly Ile Gln Val Ser Leu Tyr Cys Gln Glu Trp
172          485          490          495
174 tac gca cgg cgg cac tgc ccc tta ccc cag gca act ttc tgg ggg ctg 1536
175 Tyr Ala Arg Arg His Cys Pro Leu Pro Gln Ala Thr Phe Trp Gly Leu
176          500          505          510
178 gtg aca cct cga tct tgg tcc tgc cat acc tag 1569
179 Val Thr Pro Arg Ser Trp Ser Cys His Thr *
180          515          520
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 21
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: PCR Primer
191 <400> SEQUENCE: 4
192 tgggtccatga ctggctgtac a 21
194 <210> SEQ ID NO: 5
195 <211> LENGTH: 15
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: PCR Primer

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202 <400> SEQUENCE: 5
203 cccgggcacc aagga                                     15
205 <210> SEQ ID NO: 6
206 <211> LENGTH: 25
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: PCR Probe
213 <400> SEQUENCE: 6
214 ctacgtgtat caggatgggc tgcgg                         25
216 <210> SEQ ID NO: 7
217 <211> LENGTH: 19
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: PCR Primer
224 <400> SEQUENCE: 7
225 gaaggtgaag gtcggagtc                                 19
227 <210> SEQ ID NO: 8
228 <211> LENGTH: 20
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: PCR Primer
235 <400> SEQUENCE: 8
236 gaagatggtg atgggatttc                                20
238 <210> SEQ ID NO: 9
239 <211> LENGTH: 20
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: PCR Probe
246 <400> SEQUENCE: 9
247 caagcttccc gttctcagcc                                20
249 <210> SEQ ID NO: 10
250 <211> LENGTH: 1607
251 <212> TYPE: DNA
252 <213> ORGANISM: Mus musculus
254 <220> FEATURE:
255 <221> NAME/KEY: CDS
256 <222> LOCATION: (30)...(1607)
258 <220> FEATURE:
259 <221> NAME/KEY: unsure
260 <222> LOCATION: (176)
261 <223> OTHER INFORMATION: a, c, g or t
263 <400> SEQUENCE: 10
264 ctgtgtgctg tccgctctac actggcacc atg cag oca aag gtg ccc cag ctt  53
265                                     Met Gln Pro Lys Val Pro Gln Leu
266                                     1               5

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268 cgg agg aga gaa ggg ctg gga gag gag cag gag aag gga gcc cgt gga 101
 269 Arg Arg Arg Glu Gly Leu Gly Glu Glu Gln Glu Lys Gly Ala Arg Gly
 270 10 15 20
 272 gga gaa ggg aac gca agg aca cac gga acc cca gac ttg gtg caa tgg 149
 273 Gly Glu Gly Asn Ala Arg Thr His Gly Thr Pro Asp Leu Val Gln Trp
 274 25 30 35 40
 W-OK 276 act cga cat atg gag gct gtg aag acn cag ttt ctg gag caa gca cag 197
 277 Thr Arg His Met Glu Ala Val Lys Thr Gln Phe Leu Glu Gln Ala Gln
 278 45 50 55
 280 aga gag ttg gca gag ctg ttg gat cgg gcc cta tgg gag gct atg caa 245
 281 Arg Glu Leu Ala Glu Leu Leu Asp Arg Ala Leu Trp Glu Ala Met Gln
 282 60 65 70
 284 gct tac ccc aaa caa gac aga cct ctt ccc tcc gct gcc cca gat tct 293
 285 Ala Tyr Pro Lys Gln Asp Arg Pro Leu Pro Ser Ala Ala Pro Asp Ser
 286 75 80 85
 288 aca agc aag acc ccg gag tta cgc cct gga aaa cgg aaa gtt ttc gtc 341
 289 Thr Ser Lys Thr Pro Glu Leu Arg Pro Gly Lys Arg Lys Val Phe Val
 290 90 95 100
 292 gcc cgc aag tca ctg atc gat gag cta atg gag gtg caa cat ttc cga 389
 293 Ala Arg Lys Ser Leu Ile Asp Glu Leu Met Glu Val Gln His Phe Arg
 294 105 110 115 120
 296 acc atc tac cac atg ttc ata gcg ggc cta tgg ttc ttg atc atc agc 437
 297 Thr Ile Tyr His Met Phe Ile Ala Gly Leu Trp Phe Leu Ile Ile Ser
 298 125 130 135
 300 acc ctg gcc atc gac ttc att gat gag ggc agg ttg atg ctg gag ttt 485
 301 Thr Leu Ala Ile Asp Phe Ile Asp Glu Gly Arg Leu Met Leu Glu Phe
 302 140 145 150
 304 gac tta ctc ctc ttc agc ttc gga cag ctg ccc ttg gcg ctg atg acc 533
 305 Asp Leu Leu Leu Phe Ser Phe Gly Gln Leu Pro Leu Ala Leu Met Thr
 306 155 160 165
 308 tgg gtt ccc atg ttc ctg tat acg ctc cta gtg ccc tac cag acc ctg 581
 309 Trp Val Pro Met Phe Leu Tyr Thr Leu Leu Val Pro Tyr Gln Thr Leu
 310 170 175 180
 312 tgg ctg tgg gcc agg ccg cgc gct ggg ggt gcc tgg atg ctg ggg gcc 629
 313 Trp Leu Trp Ala Arg Pro Arg Ala Gly Gly Ala Trp Met Leu Gly Ala
 314 185 190 195 200
 316 agc ctg ggc tgc gtt ctg ctg gct gcc cac gct gtg gtg ctc tgc gtc 677
 317 Ser Leu Gly Cys Val Leu Leu Ala Ala His Ala Val Val Leu Cys Val
 318 205 210 215
 320 ctg ccg gtg cac gtg tca gtg agg cat gag ctt ccg ccc gcc tgc cgc 725
 321 Leu Pro Val His Val Ser Val Arg His Glu Leu Pro Pro Ala Ser Arg
 322 220 225 230
 324 tgc gtg ctg gtc ttt gag cag gtc aga ttg ctg atg aaa agc tac tcc 773
 325 Cys Val Leu Val Phe Glu Gln Val Arg Leu Leu Met Lys Ser Tyr Ser
 326 235 240 245
 328 ttc ctg aga gag act gtg cct ggg atc ttt tgt gtc aga cga gga aag 821
 329 Phe Leu Arg Glu Thr Val Pro Gly Ile Phe Cys Val Arg Arg Gly Lys
 330 250 255 260
 332 ggc atc agc ccc cca agt ttc tcc agc tac ctc tac ttc ctc ttc tgc 869

VERIFICATION SUMMARY

DATE: 01/15/2002

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TIME: 20:21:05

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01152002\I918026A.raw

L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10